

WO 2005/089043

PCT/GB2005/001142

Fig 1A

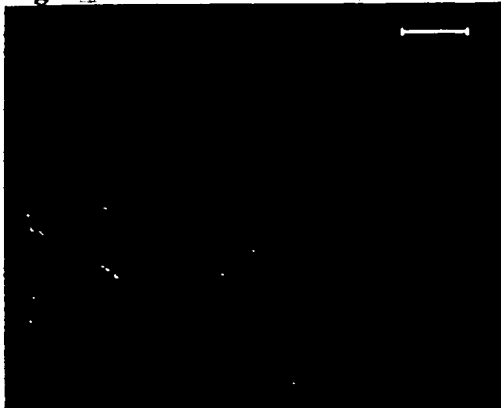


Fig 1B

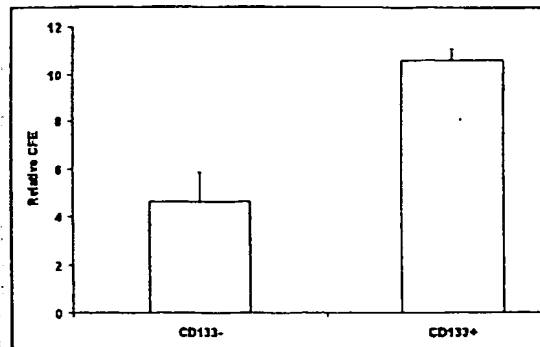
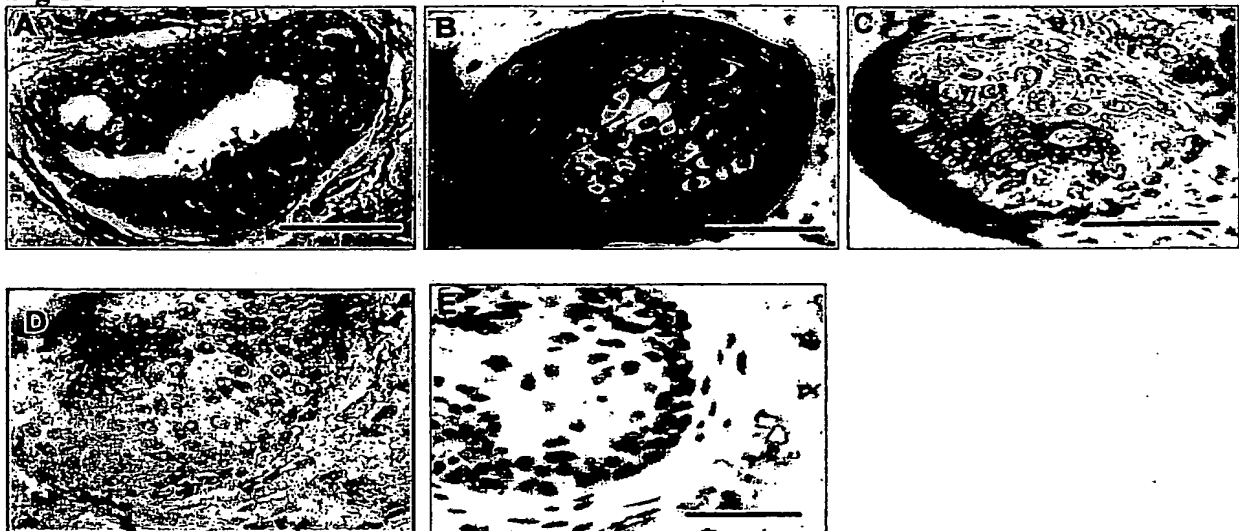


Fig 1C



WO 2005/089043

PCT/GB2005/001142

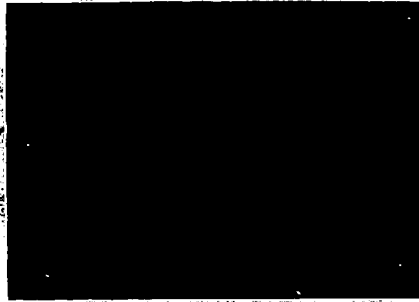
Fig 2A

2/4

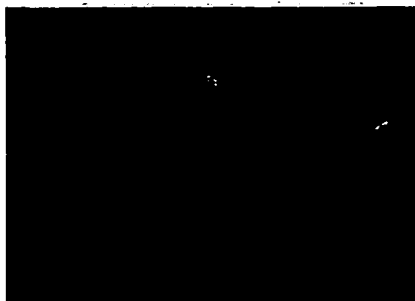
Vimentin



Cytokeratin 18



E-Cadherin



PSA



Fig 2B

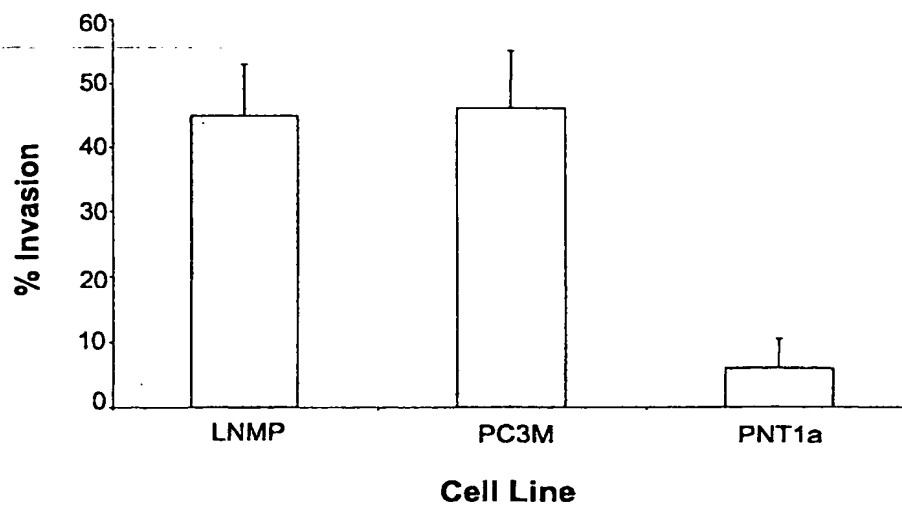


Figure 3

3/4

MHRTTRIKITELNPHLMCVLCGGYFIDATTIIECLHSFCKTCIV  
RYLETSKYCPICDVQVHKTRPLLNIIRSDKTLQDIVYKLVPGLFKNEMKRRRDFYAAHP  
SADAANGSNEDRGEVADEDKRIITDDEIISLSIEFFDQNRDRKVNKDKEKSKEEVND  
KRYLRCPAAMTVMHLRKFLRSKMDIPNTFQIDVMYEEEPKDYITLMDIAYIYTWRN  
GPLPLKYRVRPTCKRMKISHQDGLTNAGELES DSGSDKANSPAGGI PSTSSCLPSPSTPVQ  
SPHPQFPHISSTMNGTSNSPSGNHQSSFANRPRKSSVNGSSATSSG

Figure 4

4/4

```
1 CAGCAACTAT GAAATAATCG TAGTATGAGA GGCAGAGATC GGGGCGAGAC AATGGGGATG
61 TGGGCGCGGG AGCCCCGTTT CGGCTTAGCA GCACCTCCCA GCGGCGCAGA ATAAAAACCGA
121 TCGCGCCCCC TCCGCGCGCG CCCTCCCCCG AGTGCAGGAG GGGAGGAGGC GGCGGCGGCC
181 GAGGAGGAGG AGGAGGAGGC CCCGAGGAGG GAGGCGTTGG AGGTGAGGCG GGAGGCGGAG
241 GAGGAGGAGG CCGAGGCGCC GGAGGAGGCC GAGGCGCCGG AGCAGGAGGA GGCCGCGCCG
301 AGGCGGCATG AGACGAGCGT GCGGCGCGCG GCTGCTCGGG GCGGCGCTGG TTGCCCATTG
361 ACAGCGGCGT CTGCAGCTCG CTTCAAGATG GCGGCTTGGC TCGCATTTCAT TTCTGCTGA
421 ACGACTTTTA ACTTTCATTG TCTTTCCGCG CCGCTTCGAT CGCCTCGCGC CGGCTGCTCT
481 TTCCGGGATT TTTTATCAAG CAGAAATGCA TCGAACACG AGAATCAAGA TCACTGAGCT
541 AAATCCCCAC CTGATGTGTG TGCTTTGTGG AGGGTACTTC ATTGATGCCA CAACCATAAT
601 AGAATGCTTA CATTCCTTCT GTAAACGCTG TATTGTTCTG TACCTGGAGA CCAGCAAGTA
661 TTGTCTTATT TGTGATGTCC AAGTTCACAA GACCAGACCA CTACTGAATA TAAGGTCAGA
721 TAAAACTCTC CAAGATATTG TATACAAATT AGTTCAGGG CTTTTCAAAA ATGAAATGAA
781 GAGAAGAAGG GATTTTATG CAGCTCATCC TTCTGCTGAT GCTGCCAATG GCTCTAATGA
841 AGATAGAGGA GAGGTTGCAG ATGAAGATAA GAGAATTATA ACTGATGATG AGATAATAAG
901 CTTATCCATT GAATTCCTTG ACCAGAACAG ATTGGATCGG AAAGTAAACA AAGACAAAGA
961 GAAATCTAAG GAGGAGGTGA ATGATAAAAG ATACTTACGA TGCCCAGCAG CAATGACTGT
1021 GATGCACTTA AGAAAGTTTC TCAGAAGTAA AATGGACATA CCTAATACTT TCCAGATTGA
1081 TGTCATGTAT GAGGAGGAAC CTTTAAAGGA TTATTATACA CTAATGGATA TTGCTTACAT
1141 TTATACCTGG AGAAGGAATG GTCCACTTCC ATTGAAATAC AGAGTTCGAC CTACTTGTA
1201 AAGAATGAAG ATCAGTCACC AGAGAGATGG ACTGACAAAT GCTGGAGAAG TGGAAAGTGA
1261 CTCTGGGAGT GACAAGGCCA ACAGCCAGC AGGAGGTATT CCGCCAGCCT CTCTTGTTT
1321 GCCTAGCCCC AGTACTCCAG TGCAGTCTCC TCATCCACAG TTTCTCACA TTTCCAGTAC
1381 TATGAATGGA ACCAGCAACA GCGCCAGCGG TAACCACCAA TCTTCTTTTG CCAATAGACC
1441 TCGAAAATCA TCAGTAAATG GGTATCATGC AACTTCTTCT GGTGATACC TGAGACTGTT
1501 AAGGAAAAAA ATTTTAAACC CCTGATTTAT ATAGATATCT TCATGCCATT ACAGCTTCTT
1561 AGATGCTAAT ACATGTGACT ATCGTCCAAT TTGCTTCTTT TTGTAGTGAC ATTAATTTG
1621 GCTATAAAAG ATGGACTACA TGTGATACTC CTATGGACGT TAATTGAAAA GAAAGATTGT
1681 TGTTATAAAG AATTGGTTTC TTGGAAGCA GGCAAGACTT TTTCTCTGTG TTAGGAAAGA
1741 TGGGAAATGG TTTCTGTAAC CATTGTTTGG ATTTGGAAGT ACTCTGCAGT GGACATAAGC
1801 ATTGGGCCAT AGTTTGTAA TCTCAACTAA CGCCTACATT ACATTCTCTT TGATCGTTCT
1861 TGTTATTACG CTGTTTGTG AACCTGTAGA AAACAAGTGC TTTTATCTT GAAATTTAAC
1921 CAACGGAAAG AATATGCATA GAATAATGCA TTCTATGTAG CCATGTCACT GTGAATAACG
1981 ATTTCTTGCA TATTTAGCCA TTTTGATTCC TGTTTGATTT ATACTTCTCT GTTGCTACGC
2041 AAAACCGATC AAAGAAAAGT GAACTTCAGT TTTACAATCT GTATGCCTAA AAGCGGTAC
2101 TACCGTTTAT TTTACTGACT TGTTTAAATG ATTCGCTTTT GTAAGAATCA GATGGCATT
2161 TGCTTGTTGT ACAATGCCAT ATTGGTATAT GACATAACAG GAAACAGTAT TGTATGATAT
2221 ATTTATAAAT GCTATAAAGA AATATTGTGT TTCATGCATT CAGAAATGAT TGTTAAATTT
2281 CTCCCAACTG GTTCGACCTT TGCAGATACC CATAACCTAT GTTGAGCCTT GCTTACCAGC
2341 AAAGAATATT TTTAATGTGG ATATCTAATT CTAAAGTCTG TTCCATTAGA AGCAATTGGC
2401 ACATCTTTCT ATACTTTATA TACTTTTCTC CAGTAATACA TGTTTACTTT AAAAATTGTT
2461 GCAGTGAAGA AAAACCTTTA ACTGAGAAAT ATGGAAACCG TCTTAATTTT CCATTGGCTA
2521 TGATGGAATT AATATTGTAT TTTAAAAATG CATATTGATC ACTATAATTC TAAACAATT
2581 TTTTAAATAA ACCAGCAGGT TGCTAAAAGA AGGCATTTTA TCTAAAGTTA TTTTAAATAG
2641 TGGTATAGCA GTAATTTTAA ATTTAAGAGT TGCTTTTACA GTTAACAATG GAATATGCC
2701 TCTCTGCTAT GTCTGAAAAT AGAAGCTATT TATTATGAGC TTCTACAGGT ATTTTAAAT
2761 AGAGCAAGCA TGTTGAATTT AAAATATGAA TAACCCACC CAACAATTTT CAGTTTATT
2821 TTTGCTTTGG TCGAACTTGG TGTGTGTTCA TCACCCATCA GTTATTGTG AGGGTGTTTA
2881 TTCTATATGA ATATTGTTTC ATGTTTGTAT GGGAAAATTG TAGCTAAACA TTTCATTGTC
2941 CCCAGTCTGC AAAAGAAGCA CAATTCTATT GCTTTGTCTT GCTTATAGTC ATTAATCAT
3001 TACTTTTACA TATATTGCTG TFACTTCTGC TTTCTTTAAA AATATAGTAA AGGATGTTTT
3061 ATGAAGTCAC AAGATACATA TATTTTATT TTGACCTAAA TTTGTACAGT CCCATTGTAA
3121 GTGTTGTTTC TAATTATAGA TGTAATAATG AATTTTATTT GTAATTGGAA AAAATCCAAT
3181 AAAAAAGGATA TTCATTTAGA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
3241 AAAAAAAAAA A
```